

In the Specification:

Please amend the paragraph beginning at page 133, line 1 of the specification as follows:

--When the human mRNA and mouse mRNA sequences for ferritin, which each contain an IRE in the 5'-UTR, are analyzed in this manner, a plot showing the regions of sequence similarity is produced, as shown in ~~Figure 5~~ Figure 6. Pairwise analysis of the human and mouse ferritin mRNA sequences illustrate several important aspects of this type of analysis. Regions of each mRNA that encode the amino acid sequence have the highest degree of similarity, while the untranslated regions are less similar. In ~~Figure 5~~ Figure 6, the location of the IRE is indicated. In both the human and mouse ferritin mRNAs the IRES are located in the extreme 5' end of each mRNA. This demonstrates an important point -- the sequence conservation in the region of the IRE structure does not stand out against the background of sequence similarity between the human and mouse ferritin sequences. In contrast, in the comparison of human and trout (Figure 11) or human and chicken (Figure 12) ferritin mRNAs, the IRES can be immediately identified. This is because the sequence of the UTRs between human and trout or human and chicken are separated by greater evolutionary distance than human and mouse, which is logical in view of the evolutionary distance that separates humans from birds and fish compared with other mammals. Comparing the human sequence to that of birds and fish is informative because the natural drift due to evolution has allowed many sequence changes in the UTRs. However, the IRE sequences are more constrained because they form an important structure. Thus, they stand out better and can be more readily identified.--